HU

### SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Rotkreuzstiftung Zentrallaboratorium Blutspendedienst

(B) STREET: Wankdorfstrasse 10

(C) CITY Bern 22

(E) COUNTRY: Switzerland

(F) POSTAL CODE (ZIP): CH-3000

(ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity against Rhesus D antigens, DNA encoding them, complete antibodies comprising the Fab fragments and process for their preparation

(iii) NUMBER OF SEQUENCES: 64

## (iv) COMPUTER READABLE RORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-QOS/MS-DOS
- (D) SOFTWARE: PatentIn Release \\$1.0, Version \$\#1.30\$ (EPO)

(v) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/EP97X03253

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 96810421.6

(B) FILING DATE: 24-JUN-1996

# (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO



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(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: N-terminal	
<ul> <li>(vi) ORIGINAL SOURCE:</li> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor</li> <li>(D) DEVELOPMENTAL STAGE: Adult</li> <li>(E) HAPLOTYPE: Diploid</li> <li>(G) CELL TYPE: Peripheral lymphocyte B</li> </ul>	
(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA Library, LD1  (B) CLONE: LD1-40	
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: Chromosome 14</li> <li>(B) MAP POSITION: q32.3</li> <li>(C) UNITS: Chromosome band number</li> </ul>	
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295342)	
<ul> <li>(ix) FEATURE:</li> <li>(A) NAME/KEY: CDS</li> <li>(B) LOCATION:1375</li> <li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48	
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15	
TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30	96
GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	

1 1

GCA GGT ATA TGG TTT GAT GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG 192 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 50 55 60 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 70 65 75 80 CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC ACG GCT GTG TAT TAT TGT 288 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 GCG AGA GAG CGA GCA CGT GGT ATT TCT AGG TTC TAT TAC TAC ATG 336 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Met 100 105 110 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro 115 120 125 (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val

50	55	60			
Lys Gly Arg F 65	Phe Thr Ile Ser 70	Arg A	sp Asn Se 8		Гhr Leu Туг
Leu Gln Leu A	Asn Ser Leu A 90	rg Asp	Glu Asp 95	Thr Ala Va	l Tyr Tyr Cys
Ala Arg Glu A	Arg Ala Ala Ar 105	g Gly I	le Ser Arg 110	g Phe Tyr T	'yr Tyr Met
Asp Val Trp ( 115	Gly Lys Gly Th 120		al Thr Val 125	al Ser Pro	
(2) INFORMA	ATION FOR S	EQ ID	NO: 3:		
(A) LEI (B) TYI (C) STI	NCE CHARA NGTH: 318 ba PE: nucleic aci RANDEDNES POLOGY: line	ise pair id S: sing	S		
(ii) MOLEC	CULE TYPE:	cDNA 1	to mRNA		
(iii) HYPOT	HETICAL: N	0			
(iv) ANTI-S	SENSE: NO				
(v) FRAGN	MENT TYPE:	N-term	ninal		
(A) ORG (C) IND (D) DE (E) HAI (G) CEI (vii) IMMEI	NAL SOURCE GANISM: Ho DIVIDUAL IS VELOPMENT PLOTYPE: di LL TYPE: Per DIATE SOUR RARY: cDNA	mo sap OLATI TAL ST ploid ipheral CE:	E: hyperin 'AGE: Ac	lult	sus D donor
	ONE: LD1-40	•			

(viii) POSITION IN GENOME:

(B) MAP POSITION: p11

(A) CHROMOSOME/SEGMENT: Chromosome 2

(C) UNITS: Chromosome band number

<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1318</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA 48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 35 40 45
GCG TCC ACT TTG CAA AGT GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG GCA GTT TTC ACT CTC ACC ATC GCC AGT CTA CAA CCT GAA GAT 240
Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 65 70 75 80
TTT GCA ACT TAC TAC TGT CAA GAG AGT TAC AGT AAT CCT CTA ATC ACC 288
Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 85 90 95
TTC GGC CAA GGG ACA CGA CTG GAG ACT AAA  Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys  100  105

(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 45 40 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 80 75 65 70 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 90 95 85 Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-52 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5 1 TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC GCC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser 25 30 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 40

GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG 192 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 55 50 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 80 75 70 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT 288 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG 336 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 100 105 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 5 10 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser 30 20 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 45 35

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 70 75 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 110 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-52 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: P 11

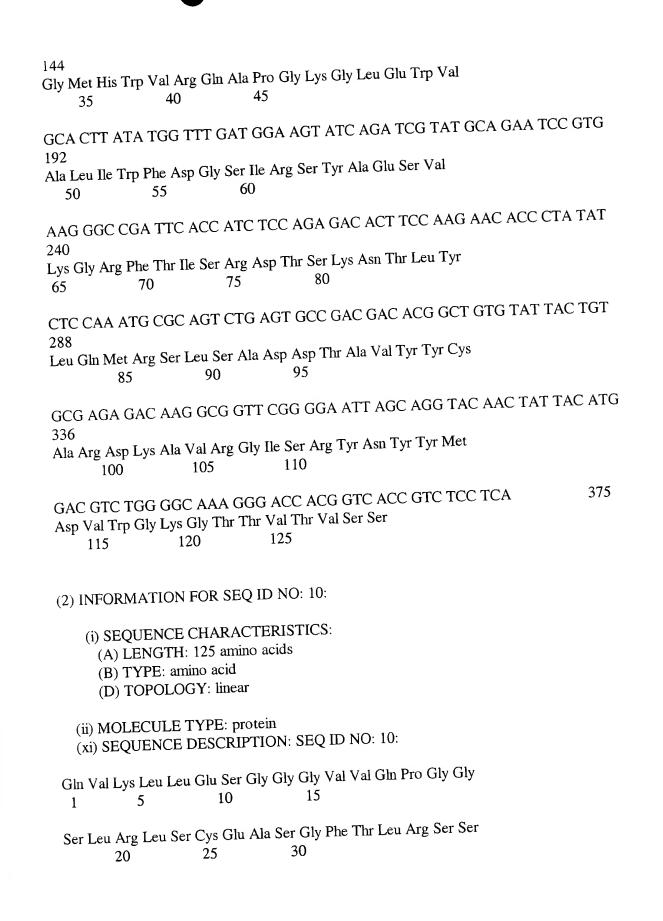
(C) UNITS: chromosome b.No
<ul><li>(ix) FEATURE:</li><li>(A) NAME/KEY: CDS</li><li>(B) LOCATION:1318</li><li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li></ul>
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA 48
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT ATC CGC TAT TTA AAT
96 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 20 25 30
TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT AGG CTC CTG ATC TAT GGT
144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly 35 40 45
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT AGT CTG CAA CCT GAA GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80
TTT GCA ACT TAC TGT CAA CAG AGT TAC CGT ACC CCT CCA TTC ACT
288 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr 85 90 95

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 1 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly 40 45 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 80 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr 95 90 85 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-84 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 5 TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 25 30 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG



Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune rhsus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-84

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGA GAC AGA 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 15 10 5 GTC ACC ATC ACC TGC CGG GCA AGT CAG AGT ATC ATC AGG TAT TTG AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 TGG TAT CAG CAC AAA CCA GGA AAA GCC CCT AAA CTC CTC ATC TTT GCT 144 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala 45 40 35 GCA TCG AAT TTG CAA ACT GGG GTC CCA TCC AGG TTC AGT GGC AGT GGA Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT GAC CTG CAG CCT GAG GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 80 75 TTC GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT AGG CCG TTC ACT TTT Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe

85 90 95

GGC CGG GGG ACC AGC CTG GAC ATC AAA Gly Arg Gly Thr Ser Leu Asp Ile Lys 100 105 315

### (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala 35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe 85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys 100 105

## (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-110 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..348) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 15 10 5 1 TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT 96 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 30 25 20

GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
144 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
GCA GGT ATA TGG TTT GAT GGA AGC AAC AAA AAC TAT GCA GAC TCC GTG
192 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 50 55 60
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC TCC AAG AAC ACT CTG TTT
<ul> <li>Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe</li> <li>70</li> <li>80</li> </ul>
CTG CAC ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT ACA TAT TAC TGT
288 Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys 85 90 95
GCG AGA GAG AGG GCG ATT CGG GGA ATC AGT AGA TAC AAT TAC TAC ATG
Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met  100 105 110
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA  Asp Val Trp Gly Lys Gly Thr Thr Val Ser Ser  115 120 125
(2) INFORMATION FOR SEQ ID NO: 14:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 125 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15
Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30

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Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe 75 70 65 Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys 95 90 85 Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 15: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-110

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: chromosome b.No (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT CGA AGC TCT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAA GTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala 40 35 GCA TCC AGT TTG CAA AGT GGG GTC CCA TCC AGG TTC AGT GGC AGA GGA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAG CCT GAA GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 TTT GCG ACT TAT TAT TGT CAA CAG AGT TCC AGT TCC TCG TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Ser Trp Thr Phe

85 90 95

GGC CAA GGG ACC AAG GTG GAA ATC AAA Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 315

#### (2) INFORMATION FOR SEQ ID NO: 16:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Ser Trp Thr Phe 85 90 95

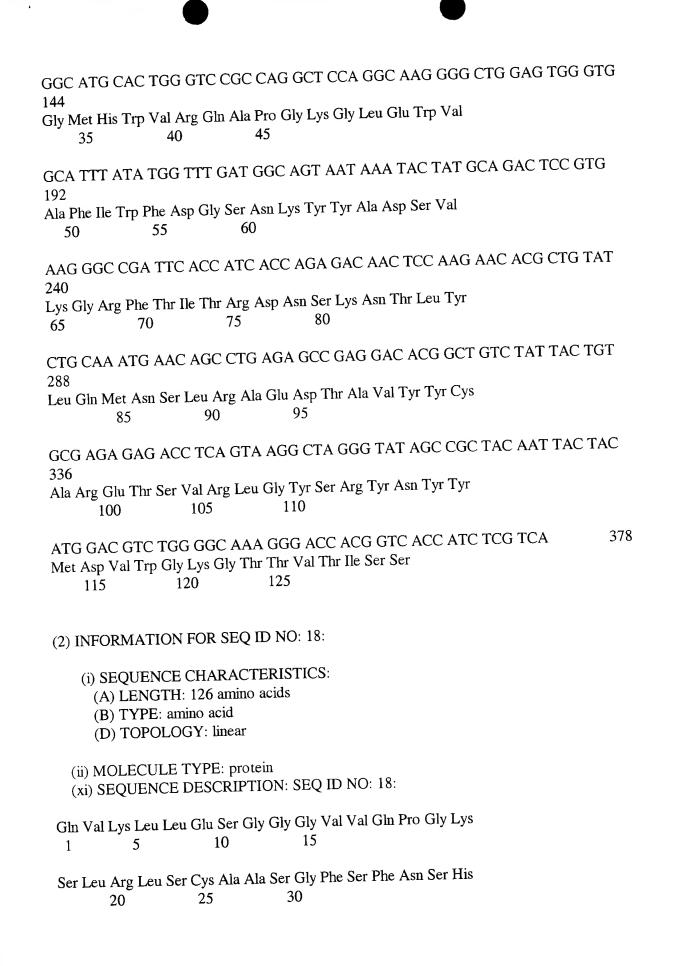
Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

### (2) INFORMATION FOR SEQ ID NO: 17:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-117 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..378 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..345) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17: CAG GTG AAA CTG CTC GAG TCA GGA GGC GTG GTC CAG CCT GGG AAG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys 5 10 1 TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTC AGT TTC AAT AGC CAT 96 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His 30 25 20



Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 60 55 Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 95 85 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr 110 105 100 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 19: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-117

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..288) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 25 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 GCA TCC AGT TTG CAA GGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 70 TTT GCA ACT TAT TAC TGT CAA CAG AGT TAC AGG GCC CCT CAG TGG ACG Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

318

#### (2) INFORMATION FOR SEQ ID NO: 20:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

#### (2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: N-terminal	
<ul> <li>(vi) ORIGINAL SOURCE:</li> <li>(A) ORGANISM: Homo sapiens</li> <li>(C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor</li> <li>(E) HAPLOTYPE: diploid</li> <li>(G) CELL TYPE: Peripheral lymphocyte B</li> </ul>	
(vii) IMMEDIATE SOURCE:  (A) LIBRARY: cDNA LIBRARY, LD2  (B) CLONE: LD2-1	
<ul> <li>(viii) POSITION IN GENOME:</li> <li>(A) CHROMOSOME/SEGMENT: chromosome 14</li> <li>(B) MAP POSITION: q32.3</li> <li>(C) UNITS: Chromosome band number</li> </ul>	
<ul> <li>(ix) FEATURE:</li> <li>(A) NAME/KEY: CDS</li> <li>(B) LOCATION:1375</li> <li>(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"</li> </ul>	
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295342)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48	
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	
TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30	96

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT
<ul> <li>Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr</li> <li>70</li> <li>80</li> </ul>
CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TGT
288 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95
GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC CTG
336 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA  Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser  115 120 125
(2) INFORMATION FOR SEQ ID NO: 22:
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 125 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmund Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA LIBRARY, LD2 (B) CLONE: LD2-1 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 22 (B) MAP POSITION: q11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..333 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(61..99, 145..165, 262..294) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23: GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGA CAG AGG GTC Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val 15 10 5 1 ACC ATC TCT TGT TCT GGA AGC AAC TCC ATC CTT GGA AGT AAG TAT GTA 96 Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val 25 20 TAC TGG TAC CAG AAA CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 45 40 35 AAG AAT GAT CAG CGG CCC TCA GGG GTC TCT GAC CGA TTC TCT GGC TCC Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 60 55 50 AAG TCT GGC ACC TCG GCC TCC CTG GCC ATC AGT GGG CTC CGG TCC GAG 240 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 80 75 70 65

GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG GAT GCC AAC CTG GGT GGC 288	
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly  85 90 95	
CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 100 105 110	333
(2) INFORMATION FOR SEQ ID NO: 24:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 111 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:	
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val 1 5 10 15	
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val 20 25 30	
Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 35 40 45	
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 50 55 60	
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 65 70 75 80	
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 85 90 95	
Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 100 105 110	
(2) INFORMATION FOR SEQ ID NO: 25:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs	

.

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD2 (B) CLONE: LD2-4 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25: CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 1

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 50 55 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 80 75 70 65 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT 288 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG 336 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 26: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 (2) INFORMATION FOR SEQ ID NO: 27: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 312 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-4 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..312 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..282) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 1 5 10 GTC ACC ATC ACT TGC CGG ACA AGT CAG ACC ATT AGC AGA AAT TTA AAT 96 Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn 25 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 ACA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 TCT GGG ACA GAT TTC ACT CTC ACC ATC AAT AGT CTA CAA CCT GAA GAT 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 75 65 TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCT TCG TTC GGC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly 95 90 85 312 CAA GGG ACC AAG GTG GAA ATC AAA Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 28: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn 25 30 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 40 45 35 Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly 90 95 85 Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-4 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15		
Ser Leu A	G AGA CTC Arg Leu Ser ( 20	TCC TGT G Cys Val Ala S 25	TA GCG T er Gly Phe 30	CT GGA TTC ACC TTC AGG AGT TAT Thr Phe Arg Ser Tyr	96
	G CAC TGO	G GTC CGC (	CAG GCT (	CCA GGC AAG GGC CTG GAG TGG GTG	
144 Gly Met 35	His Trp Val . 40			Gly Leu Glu Trp Val	
GCT TT 192	T ATA TGG	TTT GAT G	GA AGT A	AAT AAA GGA TAT GTA GAC TCC GTG	
Ala Phe	Ile Trp Phe A	Asp Gly Ser As 60	sn Lys Gly	Tyr Val Asp Ser Val	
	GC CGA TT	C ACC ATC	CC CGA	GAC AAT TCC AAG AAC ATG CTC TAT	
240 Lys Gly 65	Arg Phe Thr 70	Ile Ser Arg A 75	sp Asn Ser 80	Lys Asn Met Leu Tyr	
288				GAG GAC ACG GCT GTA TAT TAT TGT	
Leu Gln	Met Asn Ser 85	r Leu Arg Ala 90	Glu Asp Tl 95	hr Ala Val Tyr Tyr Cys	
GCG AG	GA GAG AA	G GCG CTT	CGG GGA	A ATC AGT AGA TAC AAC TAT TAC CTG	
Ala Arg	Glu Lys Ala 100	Leu Arg Gly	Ile Ser Arg 110	Tyr Asn Tyr Tyr Leu	
GAC G Asp Val	Trp Gly Lys	C AAG GGG Gly Ala Thr 120	GCC ACC Val Thr Va 125	G GTC ACC GTC TCC TCA 375 I Ser Ser	
(2) INF	ORMATION	I FOR SEQ II	) NO: 30:		
() (]					
(ii) M (xi) S	IOLECULE SEQUENCE	TYPE: protein DESCRIPTIO	n ON: SEQ II	O NO: 30:	

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 15 10 5 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 110 105 100 Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDND library. LD2 (B) CLONE: LD2-5 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..288) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGC GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 15 10 5 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC GTT ACC AGG TCT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 30 20 25 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AGG CTC CTA ATC TTT GCT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 40 35 GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 TCT GGG ACA GAT TTC ACC CTC ACC ATC AGC AGT CTG CAA CCT GAG GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 70 65

TTT GGA ACT TAC TAC TGT CAA CAG AAT TAC AGG ACC CCT CAG TGG ACG 288 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 95 90 85 TTC GGC CAA GGG ACC AAG GTA GAA ATC AAA 318 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 32: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 15 10 1 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 30 20 25 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 40 45 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 80 70 65 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 95 90 85 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-10 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..378 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 298..345) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30	96
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GT	ΓG
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GT	G
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60	
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TA	Т
240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 175 180 185	
CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TA	ΛT
288 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr 85 90 95	
TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT T	'AC
336 Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr 100 105 110	
CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	378
(2) INFORMATION FOR SEQ ID NO: 34:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 126 amino acids	

(D) TOPOLOGY: linear

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	1	0	15	
Ser Le	u Arg Lei 20	u Ser Cys 25	Val Ala S	Ser Gly Ph 30	e Thr Leu Arg Ser Tyr
	et His Trp 35	Val Arg 40	Gln Ala I	Pro Gly Ly 45	ys Gly Leu Glu Trp Val
Ala Pl 50	ne Ile Trp	Phe Asp (	Gly Ser A 60	sn Lys Gl	y Tyr Val Asp Ser Val
Lys G 65		e Thr Ile S 70	Ser Arg A 75	Asp Asn So 8	er Lys Asn Met Val Tyr 0
Leu C	Sln Met A 85		ı Arg Ala 90	Asp Asp 95	Thr Ala Val Tyr Tyr Tyr
Cys A	ala Arg Gi 100	lu Lys Ala 10		Gly Ile So	er Arg Tyr Asn Tyr Tyr
	Asp Val T 115	rp Gly Lys 120	s Gly Thr	Thr Val 7	Thr Val Ser Ser
(2) II	NFORMA	TION FO	R SEQ I	D NO: 35	:
(i)	(A) LEN (B) TYI (C) STR	NCE CHANGTH: 33 PE: nucleic RANDEDI POLOGY:	3 base pa cacid NESS: sii	irs	
(ii	) MOLEC	CULE TYI	PE: cDN	A to mRN	A
(iii	) НҮРОТ	HETICA	L: NO		
(i·	v) ANTI-S	SENSE: N	O		
(	v) FRAGI	MENT TY	PE: N-te	erminal	
(1	(A) OR (C) INI (D) DE (E) HA	NAL SOU GANISM DIVIDUA EVELOPM PLOTYP ELL TYPE	: Homo s L ISOLA IENTAL E: diploid	ATE: hype STAGE: 1	

.

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-10 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 22 (B) MAP POSITION: q11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..333 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(61..102, 148..168, 265..294) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35: GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 15 10 5 1 ACT CTC ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 30 25 20 CCA AAC TGG TTC CAG CAG AAG CCT GGA CAA GCA CCC AGG GCA CTG ATT 144 Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 40 TAT AGT ACA AAC AAA AAA CAC TCC TGG ACC CCT GCC CGG TTC TCA GGC Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly 60 50 55 TCC CTC CTT GGG GGC AAA GCT GCC CTG ACA CTG TCA GGT GTG CAG CCT Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 80 75 65 70

GAA GAC GAG GCT GAA TAT TAC TGC CTG CTC TAC TAT GGT GGT GCT CAA Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 95 90 85 CTC GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC 333 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro 110 105 100 (2) INFORMATION FOR SEQ ID NO: 36: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36: Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 15 10 5 1 Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 30 25 20 Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 45 40 35 Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly 60 55 50 Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 80 75 70 65 Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 95 90 85 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro 110 105 100 (2) INFORMATION FOR SEQ ID NO: 37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-11 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37: CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 20 25 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 55 50 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 80 75 70 65 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT 288 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 100 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 5 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid

(G) CELL TYPE: lymphocvyte (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-11 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39: GTG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA CGA GAC AGA 48 Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg 15 10 5 GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT GGC AGT TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn 20 TGG TAT CAG CAC AAA CCA GGG ACA GCC CCT AAA CTC CTG ATC TAT GCT Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 GTA TCC GCT TTG CAA AGT GGG GTC CCA TCG AGG TTC AGT GGC AGT AGA Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 65 TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT CCC CCG TAC ACT TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe 95 90 85 315 GGC CAG GGG ACC AAC CTG CAG ATC AAA Gly Gln Gly Thr Asn Leu Gln Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40: Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg 10 15 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn 30 25 20 Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 65 70 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe 95 90 85 Gly Gln Gly Thr Asn Leu Gln Ile Lys 100 105 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-14 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5 1

TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT 96 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 60 50 55 AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT 240 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 85 GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 125 115 (2) INFORMATION FOR SEQ ID NO: 42: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5		10		15	
Ser Le	u Arg Val 20	l Ala Cys 25		a Ser C 30	ily Phe	Thr Phe Arg Asn Phe
	et His Trp 35	Val Arg 40	g Gln Al	a Pro ( 45	Gly Ly	s Gly Leu Glu Trp Val
Ala Ph 50	ne Ile Trp	Phe Asp 55	Ala Ser	Asn L 60	ys Gly	Tyr Gly Asp Ser Val
Lys G		e Thr Va 70	l Ser Ar 75	g Asp	Asn S	er Lys Asn Thr Leu Tyr )
Leu G	ln Met As 85	sn Gly Le	eu Arg A 90	Ala Glu	Asp 5	Γhr Ala Val Tyr Tyr Cys
Ala A	rg Glu Ly 100		l Arg Gl 05	ly Ile S 1	er Arg 10	g Tyr Asn Tyr Tyr Met
	al Trp Gl 115	ly Lys Gl 120	y Thr T	hr Val 125	Thr V	al Ser Ser
(2) IN	IFORMA	TION FO	OR SEQ	ID N	O: 43:	
(i)	(B) TYP (C) STR	NCE CH. NGTH: 3: PE: nucle ANDED POLOGY	15 base ic acid ONESS:	pairs	rics:	
(ii)	MOLEC	ULE TY	PE: cD	NA to	mRN/	A
(iii)	НҮРОТ	HETICA	L: NO			
(iv	) ANTI-S	SENSE: 1	NO			
(v	) FRAGN	MENT T	YPE: N-	-termin	nal	
(v	(C) INI (D) DE (E) HA	GANISN	M: Homo AL ISOI MENTA PE: diplo	LATE: LL STA oid	hyper	immune Rhesus D donor dult

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(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-14 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AAC AAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn 30 25 20 TGG TAT CAG CAG AAA CCA GGC AAA GCC CCT GAA CTC CTG ATC TAT GCT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 35 GCA TCC AGT TTG CAA AGT GGG GTC CCT TCA AGG TTC CGT GGC AGT GGA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 60 55 50 TCT GGG AGA GAT TTC ACT CTC ACC GTC ACC AGT CTG CAA CCT GAA GAT Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 80 75 70 65

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 95 90 85 315 GGC CAA GGG ACC AAG GTG GAA ATC AAA Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 40 35 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 55 50 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 95 90 85 Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 45: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA llibrary (B) CLONE: LD2-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.43 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT 96 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 25 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 50 AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ACG CTC TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 80 75 70 CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 110 105 100 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	10	)	15	
Ser Le	u Arg Leu 20	Ser Cys V 25	/al Ala S	Ser Gly P 30	he Thr Phe Arg Ser Tyr
	et His Trp 35	Val Arg ( 40	Gln Ala l	Pro Gly I 45	ys Gly Leu Glu Trp Val
Ala Pł 50	ne Ile Trp	Phe Asp G 55	ly Ser A	sn Lys G	ily Tyr Val Asp Ser Val
Lys G 65		e Thr Ile S '0	er Arg A 75	Asp Asn S	Ser Lys Asn Thr Leu Tyr 80
Leu G	iln Met Ly 85		Arg Ala 00	Glu Asp 95	Thr Ala Val Tyr Tyr Cys
Ala A	rg Glu Ly 100	s Ala Leu 105		Ile Ser A	arg Tyr Asn Tyr Tyr Leu
	/al Trp Gl 115	y Lys Gly 120	Thr Thr	Val Thr 125	Val Ser Ser
(2) IN	NFORMA	TION FO	R SEQ I	D NO: 4'	7:
(i)	(A) LEN (B) TYF (C) STR	NCE CHA IGTH: 315 PE: nucleic ANDEDN POLOGY:	base pa acid IESS: sir	irs	<b>:</b> :
(ii	) MOLEC	CULE TYP	E: cDN	A to mRl	NA
(iii	) НҮРОТ	HETICAL	.: NO		
(ir	v) ANTI-S	SENSE: N	0		
(	v) FRAGN	MENT TY	PE: N-te	erminal	
(\	(A) OR (C) INI (D) DE (E) HA	NAL SOU GANISM: DIVIDUAI VELOPM PLOTYPE LLL TYPE:	Homo : L ISOLA ENTAL E: diploid	ATE: hyp STAGE d	

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(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: pl1 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47: GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA 48 Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 30 25 20 TGG TAT CAG CAG AAA CCA GGG ACA GCC CCT AAG CTC CTG ATC TAT GCT 144 Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 40 35 GCA TCC AGG TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGG Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC ACT CTG CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 80 75 70 65

TIT GCG ACT TAC TAC TGT CAA CAG AGT TAC AGT GCC CCT TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 95 90 85 315 GGC CAA GGG ACC AAG CTG GAA ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48: Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 95 90 85 Gly Gln Gly Thr Lys Leu Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 49: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library LD2 (B) CLONE: LD2-20 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10

96

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5		10		15	
Ser Le	ı Arg Leu 20	Ser Cys 25		Ser G 30	lly Phe	Thr Ser Arg Ser Tyr
	et His Trp 5	Val Arg 40	Gln Ala	Pro C 45	Gly Lys	Gly Leu Glu Trp Val
Ala Ph 50	e Ile Trp	Phe Asp 55	Gly Ser .	Asn L 0	ys Gly	Tyr Val Asp Ser Val
Lys Gl 65		e Thr Ile 0	Ser Arg 75	Asp A	sn Ser 80	Lys Asn Thr Leu Tyr
Leu G	ln Met Ly 85	s Ser Le	u Arg Al 90	a Glu	Asp T 95	hr Ala Val Tyr Tyr Cys
Ala A	rg Glu Ly 100	s Ala Lei 10	a Arg Gl 05	y Ile S 1	Ser Arg 10	Tyr Asn Tyr Tyr Leu
	al Trp Gl .15	y Lys Gly 120	y Thr Th	r Val' 125	Thr Va	al Ser Ser
(2) IN	IFORMA'	TION FO	OR SEQ	ID NO	D: 51:	
(i)	SEQUEN (A) LEN (B) TYP (C) STR (D) TOP	GTH: 31 E: nuclei	15 base p ic acid NESS: s	oairs	TICS:	
(ii)	MOLEC	ULE TY	PE: cDN	NA to	mRNA	
(iii)	НҮРОТ	HETICA	L: NO			
(iv	) ANTI-S	ENSE: 1	ON			
(v	) FRAGN	MENT T	YPE: N-	termin	al	
(v	(C) INI (D) DE (E) HA	GANISM	1: Homo AL ISOL MENTAI PE: diplo	.ATE: L STA id	hyperi GE: a	

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(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-20 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 30 25 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 40 35 GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 70 65

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CGA TTC ACT TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 95 90 85 315 GGC CCT GGG ACC AAA GTG GAT ATC AAA Gly Pro Gly Thr Lys Val Asp Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 52: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 95 90 85 Gly Pro Gly Thr Lys Val Asp Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 53: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-6-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..384 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..351) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 15 10 5



TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

GCA GAT ATA TGG TTT GAT GGA GGT AAT AAA CAT TAT GCA GAC TTC GTG 192

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT 240

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80

CTA CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTG TAT TAC TGT 288

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

GCG AGG GAT TAC TAT AGC GTT ACT AAG AAA CTC AGA CTC CAC TAC TAC 336

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110

TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 384

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 220 225 230

## (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 10 5 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 30 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 60 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 110 105 100 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult

(E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-6-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA ACC 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr 30 25 20 TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 GCA TCC AAT TTA CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 55 60 50 TCT GGC ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp TTT GCA ACT TAT TAC TGT CTA CAA GAT AAC AAT TTC CCG TAC ACT TTT Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe GGC CAG GGG ACC AAG CTG GAG ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys (2) INFORMATION FOR SEQ ID NO: 56: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys (2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 and LD2 (B) CLONE: LD1/2-6-3 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	10	15		
TCC C' Ser Leu	ΓG AGA C Arg Val A 20	GTC GCC TGT Ala Cys Val Ala 25	GTA GCG 7 Ser Gly Phe 30	TCT GGA TTC ACC TTC AGG AAT TTT Thr Phe Arg Asn Phe	96
GGC A	TG CAC	TGG GTC CGC	CAG GCT	CCA GGC AAG GGG CTG GAG TGG GTG	
Gly Me		Val Arg Gln Ala 40	Pro Gly Lys 45	Gly Leu Glu Trp Val	
GCT T 192	TT ATT T	GG TTT GAT	GCA AGT A	AAT AAA GGA TAT GGA GAC TCC GTT	
Ala Phe		he Asp Ala Ser 55 6	Asn Lys Gly 0	Tyr Gly Asp Ser Val	
AAG (	GC CGA	TTC ACC GTC	C TCC AGA	GAC AAT TCC AAG AAC ACG CTC TAT	
Lys Gly	y Arg Phe 70		g Asp Asn Se 80	r Lys Asn Thr Leu Tyr	
CTG C 288	CAA ATG	AAC GGC CTC	G AGA GCC	GAA GAC ACG GCT GTA TAT TAT TGT	
Leu G	n Met Asn 85	Gly Leu Arg A 90	la Glu Asp T 95	'hr Ala Val Tyr Tyr Cys	
GCG <i>I</i>	AGA GAG	AAG GCG GT	T CGG GG	A ATT AGT AGA TAC AAC TAC TAC ATG	
Ala Aı	g Glu Lys 100	Ala Val Arg Gl 105	y Ile Ser Arg 110	Tyr Asn Tyr Tyr Met	
GAC ( Asp V	GTC TGG al Trp Gly	Lys Gly Thr Th	ır Val Thr Va	G GTC ACC GTC TCC TCA 375 al Ser Ser	
1	15	120	125		
(2) IN	FORMAT	ION FOR SEQ	ID NO: 58:		
(i	(A) LENC (B) TYPE	NCE CHARACT GTH: 125 amino E: amino acid DLOGY: linear			
(ii) (xi)	MOLECU SEQUEN	TLE TYPE: prot ICE DESCRIPT	ein TION: SEQ I	D NO: 58:	

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 60 55 50 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 59: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 and LD2 (B) CLONE: LD1/2-6-3 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 30 25 20 TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT ACT Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr 45 35 GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 60 50 55 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe GGC CAG GGG ACC AAG CTG CAG ATC AAA Gly Gln Gly Thr Lys Leu Gln Ile Lys (2) INFORMATION FOR SEQ ID NO: 60: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Lys 

(2) INFORMATION FOR SEQ ID NO: 61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesud D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 and LD2 (B) CLONE: LD1/2-2-33 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

1	5	10	15	l Gln Pro Gly			
Ser Leu Ar 20	g Val Ala C	lys Val Ala Se 25	30	Truc Aig Asi			96
	CAC TGG	GTC CGC C	AG GCT CC	A GGC AAG	GGG CTG G	AG TGG GTG	
144 Gly Met H 35	is Trp Val A		ro Gly Lys G 5	ly Leu Glu Trj	o Val		
	ATT TGG	TTT GAT G	CA AGT AA'	T AAA GGA	TAT GGA GA	C TCC GTT	
50	55	60		r Gly Asp Ser			
	C CGA TTO	C ACC GTC	TCC AGA GA	AC AAT TCC	CAAG AAC A	CG CTC TAT	
240 Lys Gly <i>A</i> 65	arg Phe Thr 70	Val Ser Arg A	Asp Asn Ser I 80	Lys Asn Thr L	eu Tyr		
	A ATG AAG	C GGC CTG	AGA GCC G	AA GAC AC	G GCT GTA T	TAT TAT TGT	•
	85	90	95	· Ala Val Tyr '			
	GA GAG AA	G GCG GTT	CGG GGA	ATT AGT AC	GA TAC AAC	TAC TAC AT	G
	Glu Lys Ala .00	Val Arg Gly 105	Ile Ser Arg T 110	yr Asn Tyr Ty	r Met		
GAC GT Asp Val 115	Trp Gly Lys	GC AAG GGC s Gly Thr Thr 120	G ACC ACG Val Thr Val 125	GTC ACC GT Ser Ser	TCC TCA	375	
(2) INF	ORMATIO	N FOR SEQ I	D NO: 62:				
()	SEQUENCI A) LENGTI B) TYPE: a D) TOPOLO	E CHARACT H: 125 amino mino acid DGY: linear	ERISTICS: acids				

(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62: Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 55 50 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 125 115 (2) INFORMATION FOR SEQ ID NO: 63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens

(C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 and LD2 (B) CLONE: LD1/2-6-33 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63: GTG ATG ACC CAG TCT CCA TCC TTC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg 15 5 10 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 30 20 25 TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT GCT Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala 45 40 35 GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 60 55 50

